

SEQUENCE LISTING

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Darwish, Kamel El
Lindahl, Ulf
Li, Jin-Ping

<120> Glucuronyl C5-Epimerase, DNA Encoding the Same and Uses Thereof

<130> 1708.0280002

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<150> US 60/304,180

<151> 2000-12-08

<150> US 09/732,026

<151> 2000-12-08

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 1854

<212> DNA

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tgt gcg cta ttc act ttg gtc aca gta ctt ttg tgg aat aag tgt tcc 96
Cys Ala Leu Phe Thr Leu Val Thr Val Leu Leu Trp Asn Lys Cys Ser
20 25 30

agc gac aaa gca atc cag ttt cct cgg cac ttg agt agt gga ttc aga 144
Ser Asp Lys Ala Ile Gln Phe Pro Arg His Leu Ser Ser Gly Phe Arg
35 40 45

gtg gat gga tta gaa aaa aga tca gca gca tct gaa agt aac cac tat 192
Val Asp Gly Leu Glu Lys Arg Ser Ala Ala Ser Glu Ser Asn His Tyr
50 55 60

gcc aac cac ata gcc aaa cag cag tca gaa gag gca ttt cct cag gaa 240
Ala Asn His Ile Ala Lys Gln Gln Ser Glu Glu Ala Phe Pro Gln Glu
65 70 75 80

caa Cag aag gca ccc cct gtt gtt ggg ggc ttc aat agc aac ggg gga 288
Gln Gln Lys Ala Pro Pro Val Val Gly Gly Phe Asn Ser Asn Gly Gly
85 90 95

agc aag gtg tta ggg ctc aaa tat gaa gag att gac tgt ctc ata aac 336
Ser Lys Val Leu Gly Leu Lys Tyr Glu Ile Asp Cys Leu Ile Asn
100 105 110

gat gag cac acc att aaa ggg aga cga gag ggg aat gaa gtt ttc ctt 384
Asp Glu His Thr Ile Lys Gly Arg Arg Glu Gly Asn Glu Val Phe Leu
115 120 125

cca ttc act tgg gta gag aaa tac ttt gat gtt tat gga aaa gtg gtc 432
Pro Phe Thr Trp Val Glu Lys Tyr Phe Asp Val Tyr Gly Lys Val Val
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cag tat gac ggc tat gat cga ttt gaa ttc tct cat agc tat tcc aaa 480
Gln Tyr Asp Gly Tyr Asp Arg Phe Glu Phe Ser His Ser Tyr Ser Lys
145 150 155 160

gtc tat gca cag aga tca cct tat cac cct gac ggt gtg ttt atg tcc 528
Val Tyr Ala Gln Arg Ser Pro Tyr His Pro Asp Gly Val Phe Met Ser
165 170 175

ttt gaa ggc tac aat gtg gaa gtc cga gac aga gtc aaa tgt ata agt 576
Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg Val Lys Cys Ile Ser
180 185 190

gga gtt gaa ggt gtg cca tta tct acc cag tgg ggg cct caa ggc tat 624
Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro Gln Gly Tyr
195 200 205

ttc tac cca atc cag att gca cag tat ggg cta agt cat tac agc aag 672
Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His Tyr Ser Lys
210 215 220

aat cta acc gag aaa ccc cct cac ata gaa gta tat gaa aca gca gaa 720
Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr Ala Glu
225 230 235 240

gac agg gac aga aac atc aga cct aat gaa tgg act gtg ccc aag ggg 768

Asp Arg Asp Arg Asn Ile Arg Pro Asn Glu Trp Thr Val Pro Lys Gly		
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tgc ttc atg gcc agt gtg gca gac aag tct aca acc aat gtt aaa		816
Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg Ser Thr Asn Val Lys		
260	265	270
cag ttt att gct cca gaa acc agt gaa ggt gtg tct ttg cag ctg gga		864
Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly		
275	280	285
aac aca aaa gac ttc att att tca ttt gac ctc aag ctt tta aca aat		912
Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Leu Leu Thr Asn		
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ggg agt gtg tct gtg gtt ctg gag acc aca gaa aag aat cag ctc ttc		960
Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln Leu Phe		
305	310	315
act gtg cat tat gtc tca aac acc cag ctg att gct ttc aga gac agg		1008
Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Arg Asp Arg		
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Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr Val Thr		
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Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser Asn Thr		
355	360	365
aaa gct gtc aag cca acc aaa atc atg ccc aaa aag gtg gtt agg ttg		1152
Lys Ala Val Lys Pro Thr Lys Ile Met Pro Lys Lys Val Val Arg Leu		
370	375	380
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Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr Ile Ser Thr Thr		
385	390	395
400		
gcc cac atg gct gca ttc ttt gct gca agt gac tgg cta gtg agg aac		1248
Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val Arg Asn		
405	410	415
cag gat gag aaa ggt ggc tgg cca att atg gtg acc cgg aag tta ggg		1296
Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys Leu Gly		
420	425	430
gaa ggg ttt aaa tct tta gaa cca gga tgg tac tct gcc atg gca caa		1344
Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala Gln		
435	440	445
ggg caa gcc atc tct acc tta gtc agg gcc tat ctt cta acg aaa gac		1392
Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys Asp		
450	455	460
tat gta ttc ctc agt tca gct tta agg gca aca gcc cca tac aag ttt		1440
Tyr Val Phe Leu Ser Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys Phe		
465	470	475
480		
ccg tca gag cag cat gga gtt aaa gcc gtg ttc atg aat aaa cat gac		1488
Pro Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys His Asp		
485	490	495

tgg tat gaa gaa tat cca acc aca cct agc tct ttt gtt tta aat ggc 1536
Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly
500 505 510

ttt atg tat tct tta att ggg ctg tat gac cta aaa gaa aca gca ggg 1584
Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly
515 520 525

gag aca ctt ggg aaa gaa gca agg tcc ttg tac gag cgc ggc atg gaa 1632
Glu Thr Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu
530 535 540

tct ctt aaa gcc atg ctg ccc ttg tat gat act ggc tcc ggg acc atc 1680
Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile
545 550 555 560

tat gac ctc cgc cac ttc atg ctt ggc att gct ccc aac ctg gcc cgc 1728
Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Arg
565 570 575

tgg gac tat cac acc acc cac att aac cag ctg cag ctg ctc agc acc 1776
Trp Asp Tyr His Thr His Ile Asn Gln Leu Gln Leu Leu Ser Thr
560 565 590

atc gat gag tcc cca atc ttc aaa gaa ttt gtc aag agg tgg aaa agc 1824
Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp Lys Ser
595 600 605

tac ctt aaa ggc agt agg gca aag cac aac 1854
Tyr Leu Lys Gly Ser Arg Ala Lys His Asn
610 615

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<400> 2

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Ser Asp Lys Ala Ile Gln Phe Pro Arg His Leu Ser Ser Gly Phe Arg
35 40 45

Val Asp Gly Leu Glu Lys Arg Ser Ala Ala Ser Glu Ser Asn His Tyr
50 55 60

Ala Asn His Ile Ala Lys Gln Gln Ser Glu Glu Ala Phe Pro Gln Glu

65

70

75

80

Gln Gln Lys Ala Pro Pro Val Val Gly Gly Phe Asn Ser Asn Gly Gly
85 90 95

Ser Lys Val Ieu Gly Leu Lys Tyr Glu Glu Ile Asp Cys Leu Ile Asn
100 105 110

Asp Glu His Thr Ile Lys Gly Arg Arg Glu Gly Asn Glu Val Phe Leu
115 120 125

Pro Phe Thr Trp Val Glu Lys Tyr Phe Asp Val Tyr Gly Lys Val Val
130 135 140

Gln Tyr Asp Gly Tyr Asp Arg Phe Glu Phe Ser His Ser Tyr Ser Lys
145 150 155 160

Val Tyr Ala Gln Arg Ser Pro Tyr His Pro Asp Gly Val Phe Met Ser
165 170 175

Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg Val Lys Cys Ile Ser
180 185 190

Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro Gln Gly Tyr
195 200 205

Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His Tyr Ser Lys
210 215 220

Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr Ala Glu
225 230 235 240

Asp Arg Asp Arg Asn Ile Arg Pro Asn Glu Trp Thr Val Pro Lys Gly
245 250 255

Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg Ser Thr Asn Val Lys
260 265 270

Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly
275 280 285

Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Leu Leu Thr Asn
290 295 300

Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln Leu Phe
305 310 315 320

Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Arg Asp Arg
325 330 335

Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr Val Thr
340 345 350

Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser Asn Thr
355 360 365

Lys Ala Val Lys Pro Thr Lys Ile Met Pro Lys Lys Val Val Arg Leu
370 375 380

Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr Ile Ser Thr Thr
385 390 395 400

Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val Arg Asn
405 410 415

Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys Leu Gly
420 425 430

Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala Gln
435 440 445

Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys Asp
450 455 460

Tyr Val Phe Leu Ser Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys Phe
465 470 475 480

Pro Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys His Asp
485 490 495

Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly
500 505 510

Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly
515 520 525

Glu Thr Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu
530 535 540

Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile
545 550 555 560

Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Arg
565 570 575

Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu Ser Thr
580 585 590

Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp Lys Ser
595 600 605

Tyr Leu Lys Gly Ser Arg Ala Lys His Asn
610 615